

Freeze/Thaw Sample Sequence

CGACCGCTCCAAGTTCGCTGAAAGTGATGCGGACGAAGAGCTCCTGTTTAATATTCCGTT MOU-UC331 GCGGCAGGCGCGCCAAATTACGTTGCCGGAGCTGAACGGCGCGGCTGGTCTGAAGGCAAA HUM-UC331 HUM-UC331 GCACGGTCACAGCCACGGCGGGGGGTGGCTGCCGCTGCGCCGCCGAACGGGAGGAGCCGCC HUM-UC331 CGAGCAGCGCGCCTGCCCTACGGCCTGTACCTGCGCATCGACCTGGAGCGGCTGCAATG HUM-UC331 CCTTAACGAGAGCCGCGAGGGCAGCGGCCGCGCGCGTCTTCAAGCCATGGGAGGAGCGGAC HUM-UC331 TTTCAAGCCGTGGGAGGA-CGGAC MOU-UC331 CGACCGCTCCAAGTTTATTGAAAGTGATGAAGAGAGCTTCTGTTTAATATTCCATT HUM-UC331 TACGGGCAATGTCAAGCTCAAAGGCATCATTATAATGGGAGGATGATGACTCACACCC HUM-UC331 TACGTGCAATGTCAAGCTGAAAGGCGTCATCATAATGGGCGAGGATGATGACTCGCACCC MOU-UC331 CAAGCGAGCGAGCGCGATAGGGGCCGAGAGGACGCGCAGGTGGCGGCGTTGCCATGTC 120 180 240 300 360 420 9 START 330 270 390 210 150

GCCAGATCAGACCTTTAGTCTGAACCGGGATCTTACAGGAGAATTAGAGTATGCTACAAA HUM-UC331 CTCTGAGATGAGACTGTACAAGAATATTCCACAGATGTCCTTTGATGATACAGAAAGGGA HUM-UC331 CTCGGAGATGAGACTGTACAAGAACATTCCACAGATGTCATTTGATGACACAGAAAGGGA MOU-UC331 540 480 450 510

AATTICICGITITICAAAIGICIAICAICICICAAIITCAIAITICAAAAAACITCGGAGC HUM-UC331 AATCTCCAGGTTTTCAAATGTCTATCATCTTTCCATTCATATTTCAAAAAACTTTGGAGC MOU-UC331 GCCAGAGCAGACCTTCAGTCTGAACCGAGACATTACAGGAGAATTAGAATATGCTACGAA MOU-UC331 009 \* \* \*\* 570

AGATACGACAAAGGTCTTTTATATTGGCCTGAGAGGAGAGTGGACTGAGCTTCGCCGACA HUM-UC331 AGATACGACGAAGATCTTTTATATTGGCCTGCGGGAGAGTGGACTGAGCTTCGCCGGCA MOU-UC331 099 630

TGAGGTGACCATCTGCAACTATGAAGCGTCAGCCAACCCAGCAGACCACCGGGTGCATCA MOU-UC331 CGAGGTGACCATCTGCAATTACGAAGCATCTGCCAACCCAGCAGACCATAGGGTCCATCA HUM-UC331 720 069

GGTTACCCCACACACACTTTATTTCCTAAGGGCTGGCCAAGGCTCCCATAGAGGCGCT HUM-UC331 MOU-UC331 GGTCACCCCCCAGACACACTTCATTTCTTAAGGGCCAGCCGGGGCTCCCTCAGATGCGCT \*

750

840 AGAG HUM-UC331 CAAT MOU-UC331	900 GGCC HUM-UC331 GGCC MOU-UC331	960 FTTCT HUM-UC331 CTCT MOU-UC331	1020 ACAC HUM-UC331 ATGC MOU-UC331 **	1080 GGAAGATT HUM-UC331 TTTCTTGT MOU-UC331 ******	1140 GGGC HUM-UC331 SACCG MOU-UC331
840 GTGTCAGTGAAGATGTACGACTACCTGTTGGGAAGGACAAAGGGATGAGGCTCCAGAGAG GTTAGTGAAGATGTGCGACCACCTGCTGGGAAGGAAGGACAAGGA-ATGCTCCAGCAAT **** **** **** ****	AGTTGGCTGCCACAGCTCTGTCTTTGGGGGCTTGCTGCAGAAACCTGGCCCAGAAACCTGGCCAAGTTGCCTGCC	930 TACGGAAGATACGACACCACTGGGAGGGTTGTGTAGGTGCCAGGGGACCATCGTGGTTCT TGTGGAAACCGCCTCACCACCAGGAGCGGTATGGGTGCCAAGGGATAGTCTCTCT ** *** ** *** ** *** ***	1020 CTAGGGCGCTGTGGAAATTGGGTCTTGGGCTGGCTGGCATCTGGCAGTCATGGGTAACAC CTAAGGCACTGCAGAAACTGGGTCTTAGGCTGGGTGGCATCTGTCAGTCA	1050 TIGCTTTTCCAGTTAATGTGCCATGTGATTCCAAGTGTCATGTTGCTTTGTGGAAGATT TCACTT-CCCAGTC-TGTGGCCACGGGATCCCATGTGTCTTTTTGCTT-GATTTCTTGT ** ** ** ** ** ********************	1110 GTTGTGTGACTTGTTTTTTGTATTTTGTATTTTTTTTAAAGGAAACTATTTGTGGGC GTGGTTTGTCCT-TTTGTGCATCAAAAAGGATGCTTCCTTGACCG  * * * * * * * * * * * * * * * * * * *

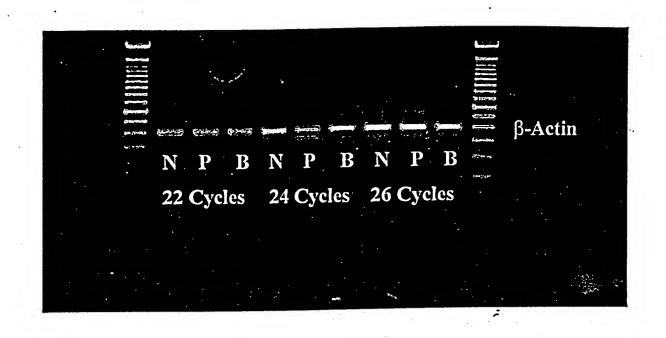
FATAGGAAACTTT FAGAATCCTT	1170 TATAGGAAACTTTCTGATGCCTCCGGATT-GTGTTAGTAGTCCCATCAGGAGGGTCTCC TAGAATCCTTCTGAAACCCG-AGTTTCGTGTTTGAATTAGCCATCAGGAGGGTCTCC * **** * * * * * * * * * * * * * * *	70 -GTGTTAGTAG CGTGTTTGAAT * * *	TAGCCATCAGGAG	1200 3GTCTCC 3GTCTCC	HUM-UC331 MOU-UC331
AACTA-AAACACT' AGCTAGAAACACT' * *	AACTA-AAACACTT-GTTCCTGCTTGCTCCTTTCCCCTCTCATTGTTCAGCATTCTTGTC AGCTAGAAACACTTCGTCCTGCTTGCTCCT-CCTCTGTCATTGCTCAGCATTCGTGTC  * * * * * * * * * * * * * * * * * * *	30 CTTTCCCCTCT CT-CCTCCTGT	CATTGTTCAGCAT: CATTGCTCAGCAT: *	1260 rcrrgrc rcgrgrc *	HUM-UC331 MOU-UC331
AAGTTGCCCAGCT AGGGTGCCTAGCT * * *	AAGTTGCCCAGCTTGGAGTTGTCTGTCACGCACATGTGTCCTGTGGTTATAGCTAGAAGGAGGTGCCTAGCTAG	1290 ACGCACATGTGTC AGACACAAGTGTC	CTGTGGTTATAGC: CCACAATGGTGGT: ***** ** *	1320 TAGAAGG TGGAAAG	HUM-UC331 MOU-UC331
ACAGGAGTCTCCT GAAGGAGTCTCCT **	ACAGGAGTCTCCTGCTGATGCGTGATAGCTTAAGCTTGGGGAGAAGGTCTTTTCCACTGCGAAGGACTCCTCTTTTCCACTGCGAAGGACTCTTTTCCACTGCAAGGAGAAGGTCTTTTCCACTGCAAAGGAAAGAAA	1350 GCTTAAGCTTGGG GCTTGGG	GAGAAGGTCTTTTC GGAAGG-CTTACA *** ***	1380 CCACTGC ACAGT-C * * *	HUM-UC331 MOU-UC331
CTAGCTAAGCAGTCTGGGGAGAGCA' TAGCCAAATTAGTT—-GCGAG **** * ** ****	1410 CTGGGGAGAGCATGGGGA TGCGAG	1410 GGGATCATTTCTA TCCTTTCCC **** * **	TGTGTGTGGGTA? TGTGTGGGTG? ** **	1440 TTCTGGTC ACCTGGTT * * *	HUM-UC331 MOU-UC331
AGTAAGATTGA GGGGTAAAACTGA * **	1470 AGTAAGATTGAGACTTAGTTAAGATTCCCCTTGGAAATTCCTTAATGTTTATTAGCTT GGGGTAAAACTGAGACAGTAAAGATTCCTCTTGGGACCTCCTTGGTGTTTCCTTGCTT * ** * * * * * * * * * * * * * * * *	1470 TCCCCTTGGAAAT TCCTCTTGGGACC	TTCCTTAATGTTTTA	1500 ATTAGCTT CCCTGCTT ****	HUM-UC331 MOU-UC331

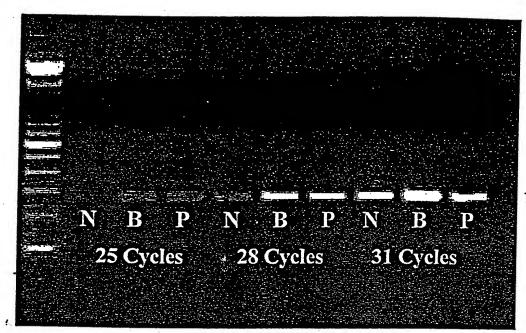
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1530	AGTCCGATGCCAGAATTTG	AACCCAGGGCTGGAGTCTG	* * * * * * * * * * * * * * * * * * * *	1590	CTAATAAGCTTCCTAATAA	CTAATGAGCTTCCTAATAA	*
	AGTGTTGTA	CATGTTATA	* **		TCACTGTGA	TCATGGTGA	*
	CTAACT	CTAACT			TTTTAI	TTTCAI	*

30 40 10 20 MSHGHSHGGGGCRCAAER-EEPPEORGLAYGLYLRIDLE HUM-UC331 >CSHGHSHN-----CAAEHIPEVPGDDVYRYDMVSYIDME ZK353.1 50 70 80 60 RLQCLNESREGSGRGVFKPWEERTDRSKFIESDADEELLF HUM-UC331 >FKPWEERTDRSKFAESDADEELLF MOU-UC331 KVTTLNESVDGAGKKVFKVMEKRDDRLEYVESDCDHELLF ZK353.1 90 120 100 110 NIPFTGNVKLKGIIIMGEDDDSHPSEMRLYKNIPOMSFDD HUM-UC331 NIPFTCNVKLKGVIIMGEDDDSHPSEMRLYKNIPOMSFDD MOU-UC331 NTPFTGHVRLTGLSIIGDEDGSHPAKIRLFKDREAMSFDD ZK353.1 140 150 160 130 TEREPDOTFSLNRDLTGELEYATKISRFSNVYHLSIHISK HUM-UC331 TEREPEQTFSLNRDITGELEYATKISRFSNVYHLSIHISK MOU-UC331 CSIEADQEIDLKQDPQGLVDYPLKASKFGNIHNLSILVDA ZK353.1 200 170 180 190 NFGADTTKVFYIGLRGEWTELRRHEVTICNYEASANPADH HUM-UC331 NFGADTTKIFYIGLRGEWTELRRHEVTICNYEASANPADH MOU-UC331 NFGEDETKIYYIGLRGEFOHEFRORIAIATYESRAQLKDH ZK353.1

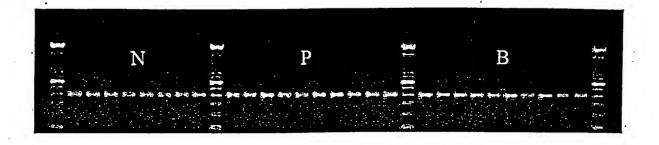
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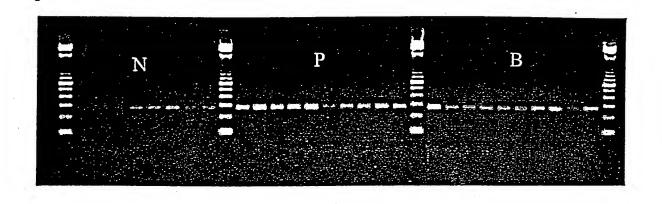
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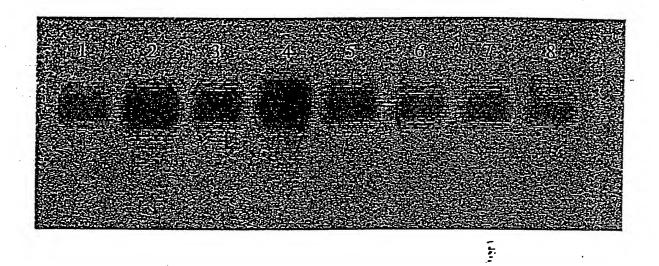




UC331





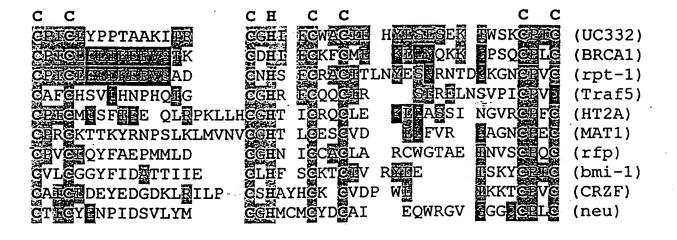


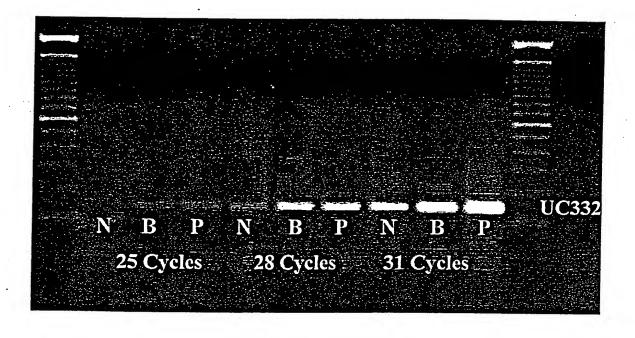
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TCC	GTTG	CTG	TGTC	GGAG.	AC A	CTAG	TCCC	C GA	CACC			CCAG	CCC	
		110			20		13			140			150	
TCT	CCCC	TGC	CTCG	CGGC	GG G	AGAG	CGTG	T CC	GGCC	GGCC	GGC	CGGC	GGG	
		160		1	70		18	0		190			200	
GCT	CGCG	CAA	CCTC	CCTC	GC C	TCCC	CTTC	c cc	CGCA	GCCT	CCG	CCCC	GCC	
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AGG	CCCG	GCC	CGGA	CTCC	CG A	GCCC	CGGC	C TC	CTCG	TCCT	CGG	TCGC	CGC	
		260			70		28			290			300	
TGC	CGCC	GGG .	CTTA	ACAG	cc c	CGTC	CGCC	G CT	TCTC	TTCC	TAG	TTTG	AGA	
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AGC			GGAA			AAAA'	TGTC	G CC	ATGA	AGGC	CGA	GAAC	CGC	
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TGC			GACC			GCCC'			CATG	AGCC	TGG	GTCC	CCG	
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CCG			TCCG			TGCC			CCGA	GGCC	CCC	GTTG	ATG	
		460		4			48			490			500	
CCG			CCCC						CTCC	GACA	TGG	ACAA	GAA	
		510			20		530			540			550	
CAG			AACA						GCAG	CAGC	AAA	GGGC	AAC	
0-10		560		5'			580			590			600	
AGC			CTCC			CGGG					TAA	ACCC	AAG	
1100		610	0100	62			630			640			650	
AGC			TAAT:						GTTG	rcag	TTG	ATTC	IGT	
1100		660			70		680			690		698		
AGT			TATG:								TAC	rctg(	3	
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ATG	ATG	GAT	GGA	AAG	AAC	TCC	AGT	GGA	TCC	AAG	CGT	TAT	AAT	740
Met	Met	Asp	Gly	Tivs	Asn	Ser	Ser	Glv	Ser	Lvs	Arg	Tvr	Asn	14
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CGC	AAA	CGT	GAA	СТТ	TCC	TAC	CCC	AAA	AAT	GAA	AGT	TTT	AAC	782
Arg	Lvs	Ara	Glu	Leu	Ser	Tvr	Pro	Lvs	Asn	Glu	Ser	Phe	Asn	28
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AAC	CAG	TCC	CGT	CGC	TCC	AGT	TCA	CAG	AAA	AGC	AAG	ACT	TTT	824
Asn	Gln	Ser	Arg	Ara	Ser	Ser	Ser	Gln	Lvs	Ser	Lvs	Thr	Phe	42
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Asn	Lvs	Met	Pro	Pro	Gln	Ara	Glv	Glv	Glv	Ser	Ser	Lys	Leu	56
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TTT														
	AGC	тст	тст	ттт	ААТ	GGT	GGA	AGA	CGA	GAT	GAG	GTA	GCA	908
Phe	AGC Ser	TCT	TCT	TTT	AAT Asn	GGT Glv	GGA Glv	AGA Ara	CGA Arg	GAT Asp	GAG Glu	GTA Val	GCA Ala	908 70
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Phe	Ser	Ser	Ser	Phe	Asn	Gly	Gly	Arg	Arg	Asp	Glu	Val	Ala	70
Phe GAG	Ser GCT	Ser CAA	Ser CGG	Phe	Asn GAG	Gly TTT	Gly AGC	Arg CCT	Arg GCC	Asp CAG	Glu TTC	Val TCT	Ala	70 950
Phe GAG	Ser GCT	Ser CAA	Ser	Phe	Asn GAG	Gly TTT	Gly AGC	Arg CCT	Arg GCC	Asp CAG	Glu TTC	Val TCT	Ala	70 950
Phe GAG Glu	Ser GCT Ala	Ser CAA Gln	Ser CGG Arg	Phe GCA Ala	Asn GAG Glu	Gly TTT Phe	Gly AGC Ser	Arg CCT Pro	Arg GCC Ala	Asp CAG Gln	Glu TTC Phe	Val TCT Ser	Ala GGT Gly	70 950 84
Phe GAG Glu CCT	Ser GCT Ala AAG	Ser CAA Gln AAG	Ser CGG Arg	Phe GCA Ala AAC	Asn GAG Glu CTG	Gly TTT Phe AAC	Gly AGC Ser CAC	Arg CCT Pro TTG	Arg GCC Ala TTG	Asp CAG Gln AAT	Glu TTC Phe TTC	Val TCT Ser	Ala GGT Gly TTT	70 950 84 992
Phe GAG Glu CCT	Ser GCT Ala AAG	Ser CAA Gln AAG	Ser CGG Arg	Phe GCA Ala AAC	Asn GAG Glu CTG	Gly TTT Phe AAC	Gly AGC Ser CAC	Arg CCT Pro TTG	Arg GCC Ala TTG	Asp CAG Gln AAT	Glu TTC Phe TTC	Val TCT Ser	Ala GGT Gly TTT	70 950 84 992
Phe GAG Glu CCT Pro	Ser GCT Ala AAG Lys	CAA Gln AAG Lys	Ser CGG Arg ATC Ile	Phe GCA Ala AAC Asn	Asn GAG Glu CTG Leu ACG	Gly TTT Phe AAC Asn GGT	Gly AGC Ser CAC His	Arg CCT Pro TTG Leu TTT	Arg GCC Ala TTG Leu GAA	Asp CAG Gln AAT Asn GGC	Glu TTC Phe TTC Phe	TCT Ser ACT Thr	GGT Gly TTT Phe CAT	70 950 84 992 98
Phe GAG Glu CCT Pro	Ser GCT Ala AAG Lys	CAA Gln AAG Lys	Ser CGG Arg ATC	Phe GCA Ala AAC Asn	Asn GAG Glu CTG Leu ACG	Gly TTT Phe AAC Asn GGT	Gly AGC Ser CAC His	Arg CCT Pro TTG Leu TTT	Arg GCC Ala TTG Leu GAA	Asp CAG Gln AAT Asn GGC	Glu TTC Phe TTC Phe	TCT Ser ACT Thr	GGT Gly TTT Phe CAT	70 950 84 992 98

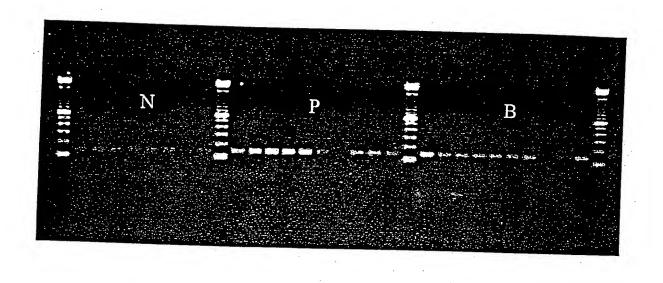
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CAA CTG GTG CT GCT CCC TTG GCG AAG GAG GTT TTT 1790 Gln Leu Val Leu Met Ala Pro Leu Ala Lys Glu Ser Val Phe 364 CAA CCC AGG AAG GGT GTG CTG GAG TAT CTG TCT GCC TTC GAT 1832 Gln Pro Arg Lys Gly Val Leu Glu Tyr Leu Ser Ala Phe Asp 378 GAA GAA ACC ACG GAA GTT TGT TCT CTG GAC ACT CCT TCT AGA 1874 Glu Glu Thr Thr Glu Val Cys Ser Leu Asp Thr Pro Ser Arg 392 CCT CTT GCT CTC CCT CTG GTA GAA GAG GAG GAA GCA GTG TCT 1916 Pro Leu Ala Leu Pro Leu Val Glu Glu Glu Ala Val Ser 406 GAA CCA GAG CCT GAG GGG TTG CCA GAG GCC TGT GAT GAC TTG 1958 Glu Pro Glu Pro Glu Gly Leu Pro Glu Ala Cys Asp Asp Leu 420 GAG TTA GCA GAT GAC AAT CTT AAA GAG GGG ACC ATT TGC ACT 2000 Glu Leu Ala Asp Asp Asn Leu Lys Glu Gly Thr Ile Cys Thr 434 GAG TCC AGC CAG CAG GAA CCC ATC ACC AAG TCA GGC TTC ACA 2042 Glu Ser Ser Gln Gln Glu Pro Ile Thr Lys Ser Gly Phe Thr 448 CGC CTC AGC AGC TCT CCT TGT TAC TAC TTT TAC CAA GCG GAA 2084 Arg Leu Ser Ser Pro Cys Tyr Tyr Phe Tyr Gln Ala Glu 462 GAT GGA CAG CAT ATG TTC CTG CAC CCT GTG AAT GTG CGC TGC 2126 Asp Gly Gln His Met Phe Leu His Pro Val Asn Val Arg Cys 476 CTC GTG CGG GAG TAC GGC AGC CTG GAG AGG AGC CCC GAG AAG 2168 Leu van vas Gin hys Chwiser hen Cibrates Sen Pro Christos 490 ATC TCA GCA ACT GTG GTG GAG ATT GCT GGC TAC TCC ATG TCT 2210 The Ser Alexander Ala Gly Tyr Ser Met Ser 504 GAG GAT GTT CGA CAG CGT CAC AGA TAT CTC TCT CAC TTG CCA 2252 Glu Asp Val Arg Gln Arg His Arg Tyr Leu Ser His Leu Pro 518 CTC ACC TGT GAG TTC AGC ATC TGT GAA CTG GCT TTG CAA CCT 2294 Leu Thr Cys Glu Phe Ser Ile Cys Glu Leu Ala Leu Gln Pro 532 CCT GTG GTC TCT AAG GAA ACC CTA GAG ATG TTC TCA GAT GAC 2336 Pro Val Val Ser Lys Glu Thr Leu Glu Met Phe Ser Asp Asp 546 ATT GAG AAG AGG AAA CGT CAG CGC CAA AAG AAG GCT CGG GAG 2378 Ile Glu Lys Arg Lys Arg Gln Arg Gln Lys Lys Ala Arg Glu 560 GAA CGC CGC CGA GAG CGC AGG ATT GAG ATA GAG GAG AAC AAG 2420 Glu Arg Arg Glu Arg Arg Ile Glu Ile Glu Glu Asn Lys 574 AAA CAG GGC AAG TAC CCA GAA GTC CAC ATT CCC CTC GAG AAT 2462 Lys Gln Gly Lys Tyr Pro Glu Val His Ile Pro Leu Glu Asn 588

GCC TTC AAT TCT TAT ACC TG CTA CAG CAG TTT Leu Gln Gln Phe Pro Ala Phe Asn Ser Tyr Thr Cys Ser Ser 602 GAT TCT GCT TTG GGT CCC ACC AGC ACC GAG GGC CAT GGG GCC 2546 Asp Ser Ala Leu Gly Pro Thr Ser Thr Glu Gly His Gly Ala 616 CTC TCC ATT TCT CCT CTC AGC AGA AGT CCA GGT TCC CAT GCA 2588 Leu Ser Ile Ser Pro Leu Ser Arg Ser Pro Gly Ser His Ala 630 GAC TTT CTG CTG ACC CCT CTG TCA CCC ACT GCC AGT CAG GGC 2630 Asp Phe Leu Leu Thr Pro Leu Ser Pro Thr Ala Ser Gln Gly 644 AGT CCC TCA TTC TGC GTT GGG AGT CTG GAA GAA GAC TCT CCC 2672 . Ser Pro Ser Phe Cys Val Gly Ser Leu Glu Glu Asp Ser Pro 658 TTC CCT TCC TTT GCC CAG ATG CTG AGG GTT GGA AAA GCA AAA 2714 Phe Pro Ser Phe Ala Gln Met Leu Arg Val Gly Lys Ala Lys 672 GCA GAT GTG TGG CCC AAA ACT GCT CCA AAG AAA GAT GAG AAC 2756 Ala Asp Val Trp Pro Lys Thr Ala Pro Lys Lys Asp Glu Asn 686 AGC TTA GTT CCT CCT GCC CCT GTG GAC AGC GAC GGG GAG AGT 2798 Ser Leu Val Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser 700 GAT AAT TCA GAC CGT GTT CCT GTG CCC AGT TTT CAA AAT TCC 2840 Asp Asn Ser Asp Arg Val Pro Val Pro Ser Phe Gln Asn Ser 714 TTC AGC CAA GCT ATT GAA GCA GCC TTC ATG AAA CTG GAC ACA 2882 Phe Ser Gln Ala Ile Glu Ala Ala Phe Met Lys Leu Asp Thr 728 CCA GCT ACT TCA GAT CCC CTC TCT GAA GAG AAA GGA GGA AAG 2924 Pro Ala Thr Ser Asp Pro Leu Ser Glu Glu Lys Gly Gly Lys 742 AAA AGA AAA AAA CAG AAA CAG AAG CTC CTG TTC AGC ACC TCA 2966 Lys Arg Lys Lys Gln Lys Gln Lys Leu Leu Phe Ser Thr Ser 756 GTC GTC CAC ACC AAG TGA CACTACTGG CCCAGGCTAC CTTCTCCATC 3013 761 Val Val His Thr Lys Stop TGGTTTTTGT TTTTGTTTTT TTTTCCCCCA TGCTTTTGTT TGGCTGCTGT 3063 AATTTTTAAG TATTTGAGTT TGAACAGATT AGCTCTGGGG GGAGGGGGTT 3113 TCCACAATGT GAGGGGGAAC CAAGAAAATT TTAAATACAG TGTATTTTCC 3163 3205 AGCTTCCTGT CTTTACACCA AAATAAAGTA TTGACACAAG AG







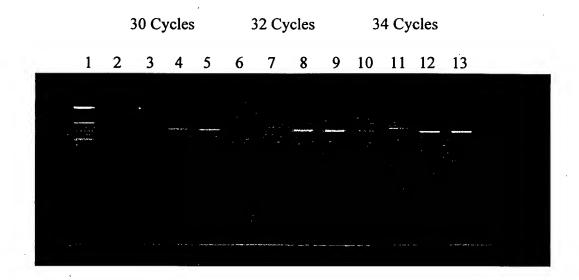


FIG. 14

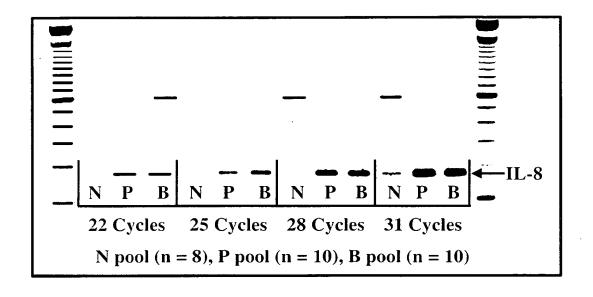


FIG. 1A

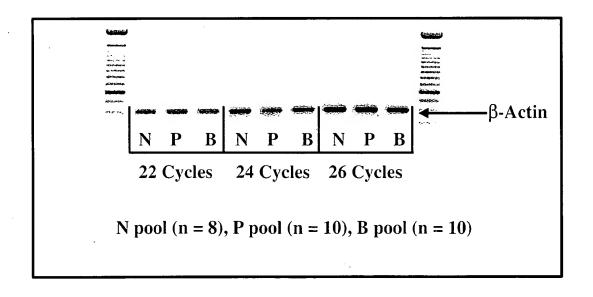


FIG. 1B

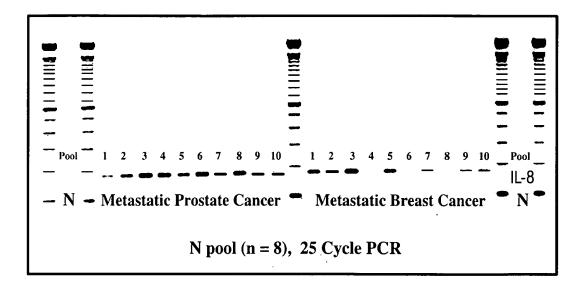


FIG. 2A

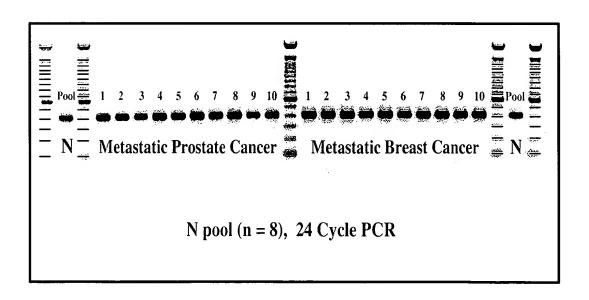


FIG. 2B

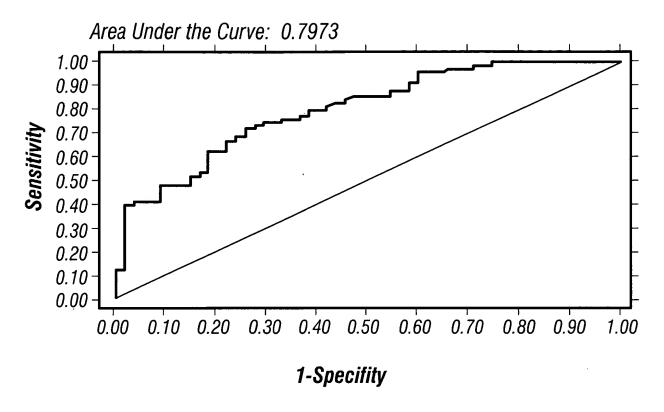


FIG. 3

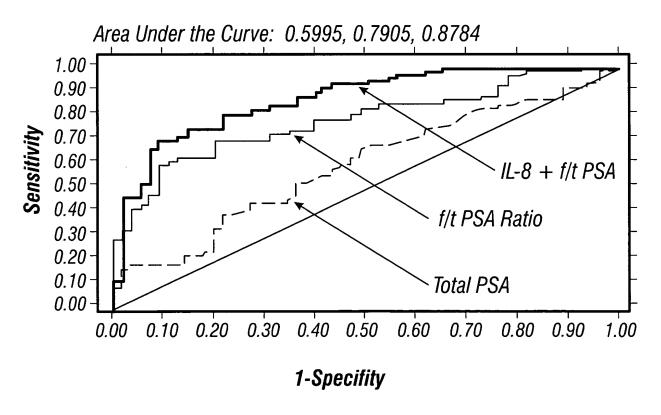
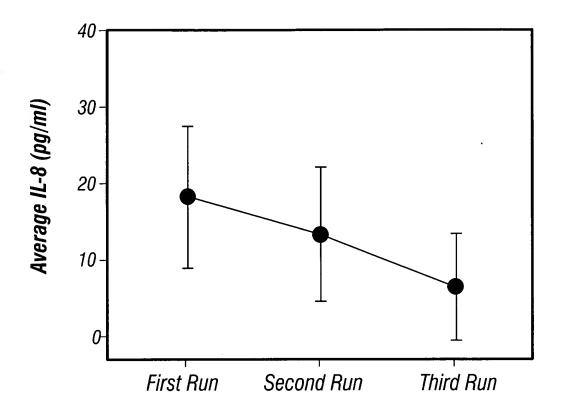


FIG. 4



Freeze/Thaw Sample Sequence

FIG. 5

C331	C331	C331	C331	C331	C331
C331	C331	C331	C331	C331	C331
HUM-UC33	HUM-UC33	HUM-UC33	HUM-UC33	HUM-UC33	HUM-UC33
MOU-UC33	MOU-UC33	MOU-UC33	MOU-UC33	MOU-UC33	MOU-UC33
510 GGGATCTTACAGGAGAATTAGAGTATGCTACAAA GAGACATTACAGGAGAATTAGAATATGCTACGAA * **	570 ATCTCTCAATTCATATTTCAAAAAACTTCGGAGC ATCTTTCCATTCATATTTCAAAAAACTTTGGAGC ** * * *	630 AGATACGACAAAGGTCTTTTATATTGGCCTGAGAGGAGAGTGGACTGAGCTTCGCCGACA AGATACGACGAAGATCTTTTATATTGGCCTGCGGGGAGAGTGGACTGAGCTTCGCCGGCA  * * * *	690 CATCTGCCAACCCAGACCATAGGGTCCATCA CGTCAGCCAACCCAGACCACAGGGTGCATCA * * *	780 GGTTACCCCACACACACTTTATTTCCTAAGGGCTGGCCAAGGCTCCCATAGAGGCGCT GGTCACCCCGCAGACACACTTCATTTCTTAAGGGCCAGGCCGGGGCTCCCTCAGATGCGCT  * * * * * * * * * * * * * * * * * * *	810 GTGTCAGTGAAGATGTACGACTACCTGTTGGGAAGGACAAAGGGATGAGGCTCCAGAGAG GTTAGTGAAGATGTGCGACCACCTGCTGGGAAGGACAGAGG-ATGCTCCAGCAAT * * * * * * * * * * * * * * * * * * *
GCCAGATCAGACCTTTAGTCTGAACC GCCAGAGCAGACCTTCAGTCTGAACC	AATTTCTCGTTTTTCAAATGTCTATC AATCTCCAGGTTTTCAAATGTCTATC * * *	AGATACGACAAAGGTCTTTTATATT AGATACGACGAAGATCTTTTATATT	CGAGGTGACCATCTGCAATTACGAAG TGAGGTGACCATCTGCAACTATGAAG *	GGTTACCCCACAGACACACTTTATT' GGTCACCCGCAGACACACTTCATT' * * *	GTGTCAGTGAAGATGTACGACTACC' GTTAGTGAAGATGTGCGACCACC' **** ****

ਜ ਜ		ਜ ਜ	н н		н н
JC33; JC33;	JC33:	JC33.	JC33.	JC33.	JC33.
HUM-UC33 MOU-UC33	HUM-UC331 MOU-UC331	HUM-UC33 MOU-UC33	HUM-UC33 MOU-UC33	HUM-UC331 MOU-UC331	HUM-UC33 MOU-UC33
AGTTGGCTGCCACAGCTCTG-CCAAGCTTTGTCTTTGGGGCTTGCTGCAGAAACCTGGCC AGTTGCCTGCCAGAGCTTTGCTTT	930 TACGGAAGATACGACACCACTGGGAGGGTTGTGTAGGTGCCAGGGGACCATCGTGGTTCT TGTGGAAACCGCCTCACCACCAGGAGCGGTATGGGTGCCAAGGGATAGTCTCTCT ** *** ** *** *** ***	1020 CTAGGGCGCTGTGGAAATTGGGTCTTGGGCTGGCTTCTGGCAGTCATGGGTAACAC CTAAGGCACTGCAGAAACTGGGTCTTAGGCTGGGTGGCATCTGTCAGTCA	1050 TTGCTTTTCCAGTTAATGTGGCCATGTGATTCCAAGTGTCATGTTGCTTTGTGGAAGATT TCACTT-CCCAGTCTGTGGCCACGGGATCCCATGTGTCTTTTTGCTT-GATTTCTTGT ** ** ** ** ** ** ** ** ** ** ** ** **	1110 GTTGTGTGACTTGTTTTTTTTTTTTTTTTTTTTTTTTTT	1170 TATAGGAAACTTTCTGATGCCTCCGGATT-GTGTTAGTAGTAGCCATCAGGAGGGTCTCC TAGAATCCTTCTGAAACCCG-AGTTTCGTGTTTGAATTAGCCATCAGGAGGGTCTCC * **** * * * * * * * * * * * * * * *

HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331
AACTA-AAACACTT-GTTCCTGCTTGCTCCTTTCCCCTCTCATTGTTCAGCATTCTTGTC AGCTAGAAACACTTCGTCCTTGCTCCT-CCTCTGTCATTGCTCGTGTC  * * * * * * * * * * * * * * * * * * *	1290 AAGTTGCCCAGCTTGGAGTTGTCTGTCACGCACATGTGTCCTGTGGTTATAGCTAGAAGG AGGGTGCCTAGCT-GGTGTCACATATCAGACACAAGTGTCCCACAATGGTGGTTGGAAAG * * * * * * * * * * * * * * * * * * *	ACAGGAGTCTCCTGCTGATGCGTGATAGCTTAAGCTTGGGGAGAAGGTCTTTTCCACTGC GAAGGAGTCTCCTGATACATGACTGCTTGGGGAAGG-CTTACACAGT-C ** ** ** ** ** ** ** ** ** ** ** ** **	1410 CTAGCTAAGCAGTCTGGGGAGCATGGGGATCATTTCTATGTGTGGGTAATCTGGTC TAGCCAAATTAGTTGCGAGTCCTTTCCCTGTGTGGGTGACCTGGTT **** * ** ** ** ** ** ** ** ** ** ** **	AGTAAGATTGAGACTTAAGATTCCCCTTGGAAATTCCTTAATGTTTATTAGCTT GGGGTAAAACTGAGACAGATTCCTCTTGGGACCTCCTTGGTGTTTCCTGCTT  * ** * * * * * * * * * * * * * * * *	1530 CTAACTAGTGTTGTAAGTCCGATGCCAGAATTTGGAGATTTGAGTTCTTTTTTTT

	HUM-UC331	MOU-UC331	
1620	AGACTTAAAAAAAAAA	AGACTTAAAA	
1590	TITIATICACIGIGACTAATAAGCTICCTAATAAATCCTIGCCAGACTTAAAAAAAAAA	TTTCATTCATGGTGACTAATGAGCTTCCTAATAAATCCTTAG-AGACTTAAAA	*
	<b>3ACTAATAA</b> G	SACTAATGAG	*
	<b>LCACTGT</b>	<b><i>ICATGGT</i></b>	* *
	TTTTAT"	TTTCAT"	*

10	20	30	40	
MSHGHSHGG	GGCRCAAER-I	EEPPEQRGLA	YGLYLRIDLE	HUM-UC331
>CSHGHSHN-	CAAEHII	PEVPGDDVYR	YDMVSYIDME	ZK353.1
50	60	70	80	
RLQCLNESRE	GSGRGVFKPWI	EERTDRSKFI	ESDADEELLF	HUM-UC331
	>FKPWI	EERTDRSKFAI	ESDADEELLF	MOU-UC331
KVTTLNESVD	GAGKKVFKVMI	EKRDDRLEYVI	ESDCDHELLF	ZK353.1
90	100	110	120	
NIPFTGNVKL	KGIIIMGEDDI	DSHPSEMRLY	KNIPQMSFDD	HUM-UC331
NIPFTCNVKL	KGVIIMGEDDI	DSHPSEMRLYI	KNIPQMSFDD	MOU-UC331
NIPFTGHVRL	TGLSIIGDED	GSHPAKIRLFI	KDREAMSFDD	ZK353.1
130	140	150	160	
TEREPDQTFS	LNRDLTGELE	YATKISRFSN	VYHLSIHISK	HUM-UC331
TEREPEQTFS	LNRDITGELE	YATKISRFSN	VYHLSIHISK	MOU-UC331
CSIEADQEID	LKQDPQGLVD'	YPLKASKFGN	IHNLSILVDA	ZK353.1
170	180	190	200	
NFGADTTKVF	YIGLRGEWTE	LRRHEVTICN	YEASANPADH	HUM-UC331
NFGADTTKIF	YIGLRGEWTE	LRRHEVTICN	YEASANPADH	MOU-UC331
NFGEDETKIY	YIGLRGEFQHI	EFRQRIAIAT:	YESRAQLKDH	ZK353.1
0.4.0				

RVHQVTPQTHFIS. HUM-UC331 RVHQVTPQTHFIS. MOU-UC331 KNEIPDAVAKGLF. ZK353.1

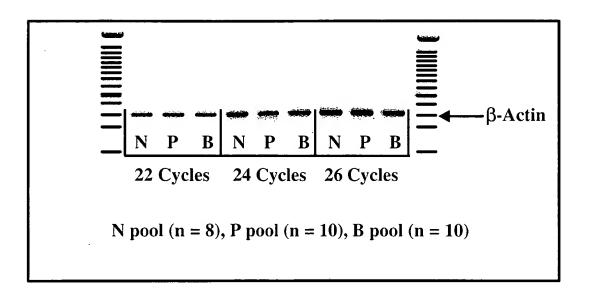


FIG. 8A

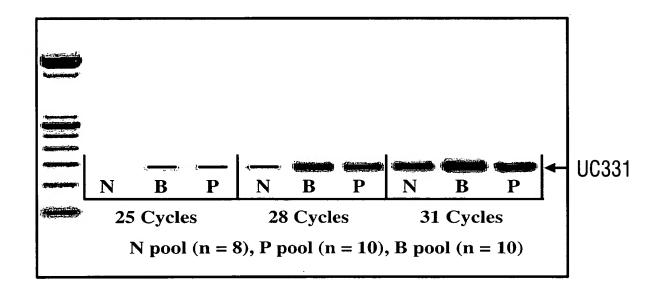


FIG. 8B

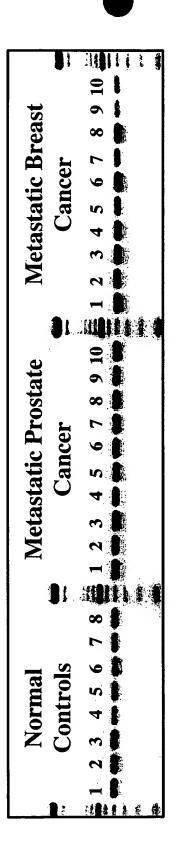


FIG. 9A

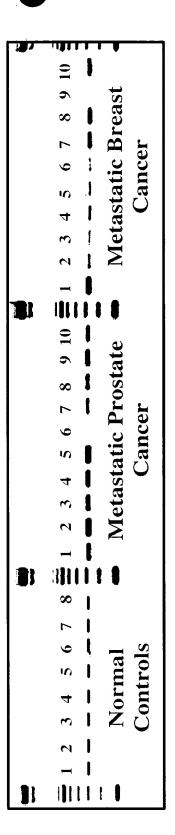


FIG. 9B

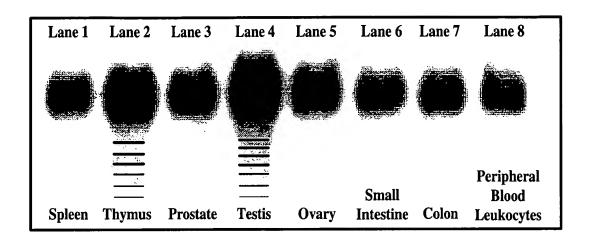


FIG. 10

50 GGGGCGAGTA 100 CAGCCAGCCC	150 GGCCGGCGGG	CCGCCCCGCC 250 CGGTCGCCGC	TAGTTTGAGA 350 CGAGAACCGC 400	TGGGTCCCCG 450 CCCGTTGATG 500	TGGACAAGAA 550 AAAGGGCAAC 600 TAAACCCAAG
40 CCTCGGCCCA 90 GACACCGAGA	140 CCGGCCGGCC 190	CCCGCAGCCT 240 TCCTCGTCCT 290	CTTCTCTTCC 340 CCATGAAGGC 390	GCCATGAGCC 440 CGCCGAGGCC 490	GCCTCCGACA 540 GGGCAGCAGC 590 CCGGCGAGTC
30 AGCAGGTCGG 80 ACTAGTCCCC	130 GAGAGCGTGT 180	CTCCCCTTCC 230 AGCCCCGGCC	CCGTCCGCCG 330 AAAAATGTCG 380	GGCCCTGAAC 430 CTGCCGTCGC	CGCCGCCACC 530 CCGCCTCTTC 580 GCGGGGCCAG
20 CCATTCCCGG 70 TGTCGGAGAC	120 CTCGCGGCGG	CCTCCCTCGC 220 CGGACTCCCG	CTTAACAGCC 320 GGAAACAGGG 370	GACCCCGCC 420 TCCGCTCCGA 470	CCCCCAACGC 520 AACAGCTCCT 570 CTCCGCCTCG
10 CGACTCGTCG 60 TCCGTTGCTG	110 TCTCCCCTGC	GCTCGCGCAA 210 AGGCCCGGCC	TGCCGCCGGG 310 AGCCAAGGAA 360	TGCCGCCGCC 410 CCGCGCCGC	CCGCTGAGCT 510 CAGCGGCTCC 560 AGCCGCCCCG

	740 14	782 28	824 42	866 56	908	950 84	992
							$\sigma$
650 TGT 8 G	AAT Asn	AAC Asn	TTT Phe	CTC	GCA Ala	GGT	TTT Phe
6 TTCT 698	$\mathtt{TAT}$	TTT Phe	ACT Thr	AAA Lys	GTA Val	TCT Ser	ACT Thr
650 TTGATTCTGT 698 TACTCTGG	CGT Arg	AGT Ser	AAG Lys	AGC Ser	GAG Glu	TTC Phe	TTC Phe
640 CAG 690 AAC	AAG Lys	GAA Glu	AGC Ser	AGC Ser	GAT Asp	CAG Gln	AAT Asn
640 TTGTTGTCAG 690 GCTTGTCAAC	TCC Ser	AAT Asn	AAA Lys	GGC Gly	CGA Arg	GCC Ala	TTG Leu
	GGA	AAA Lys	CAG Gln	GGC Gly	AGA Arg	CCT Pro	TTG Leu
630 CAAT 680	AGT Ser	CCC Pro	TCA Ser	GGC Gly	GGA Gly	AGC Ser	CAC His
630 TGGATTCAAT 680 CTCTGGAGGT	TCC Ser	$\mathtt{TAC}$	AGT Ser	AGG Arg	GGT Gly	TTT Phe	AAC Asn
_	AAC Asn	TCC Ser	TCC Ser	CAA Gln	AAT Asn	GAG Glu	CTG Leu
620 TAATTTCAGC 670 TATGTTGCCC	AAG Lys	CTT Leu	CGC Arg	CCT	TTT Phe	GCA Ala	AAC Asn
TAATT	GGA Gly	GAA Glu	CGT	CCT	TCT Ser	CGG Arg	ATC Ile
	GAT Asp	CGT	TCC Ser	ATG Met	TCT Ser	CAA CGG Gln Arg	
610 AGCGAATTAC 660 AGTAAGGCCA	ATG Met	AAA Lys	CAG Gln	AAG Lys	AGC Ser	GCT Ala	AAG AAG Lys Lys
AGCC AGT?	ATG Met	CGC Arg	AAC Asn	AAC Asn	TTT Phe	GAG Glu	CCT

1370	224
GAT	Asp
AAG	Lys
AAG 1	Lys
CAT	His
GIG	Val
$_{ m LCI}$	Ser
AGT	Ser
TAC AGT	Tyr
TGT	Cys
ATC	Ile
CCC	$\operatorname{Pro}$
$\mathtt{TGT}$	Cys
AAA	Lys
AGT	Ser

1412	238
GTT	Val
GLI	Val
$\mathtt{TAT}$	Tyr
CAG	Gln
CAT	His
$\mathtt{TCA}$	Ser
GAG	Glu
ACA	$\operatorname{Thr}$
GCC	Ala
$_{ m GLL}$	Val
$\mathtt{GTL}$	Val
AGT	Ser
AAG	Lys
CIC	Leu

1706 gcc Ala  $_{
m LLG}$ Len GlyGGA TCG Ser Leu CIG Ala GCT GAG Glu Glu GAA Arg CGG  $\operatorname{Thr}$ ACT AAG LysCICLeu Glu GAG CAG Gln

1748 350 GAA Glu Leu CIG GCT Ala GCT Ala GIG ValGLL Val G1yGGT ACT  $\mathtt{Thr}$ GIC Val Glu GAG AGG Arg AGA Arg AGC Ser GGA Gly

1790 364 Phe TTTGTT Val Ser TCT GAG Glu AAG Lys GCG Ala TTGLeu Pro CCC GCT Ala ATG Met Leu CIG GTG Val CIG Leu CAA Gln

1832 378 Asp GAT  $_{
m LLC}$ Phe gaa Ala  $_{
m LCI}$ Ser CIG Len TAT TyrGAG CIG Leu GTG Val GGT Gly AAG LysAGG Arg CCC Pro CAA Gln

392 Arg AGA  $\mathtt{TCT}$ Ser CCIPro  $\operatorname{Thr}$ ACT GAC Asp CTG Leu  $_{
m LCI}$ Ser  $_{\mathrm{TGT}}$ CysGLLVal GAA Glu ACG Thr ACC Thr Glu GAA GAA Glu

1916 406 TCT Ser GTGVal GCA Ala Glu GAA GAG Glu GAG Glu GAA Glu GTA Val CTG Len Pro CCT CIC Len GCT Ala Leu CTT Pro CCT

1958 420  $_{
m TTG}$ Leu Asp GAC GATAsp  $_{\mathrm{IGI}}$ Cys BCC Ala GAG Glu CCA Pro  $_{
m LLG}$ Leu 9999 GlyGAG Glu CCIPro GAG Glu CCA Pro GAA Glu

2000 ACT  $\operatorname{Thr}$  $_{
m LGC}$ CysATT ACC  $\operatorname{Thr}$ GGG Gly GAG Glu AAA LysCTTLen AAT Asn Asp GAC Asp GAT Ala GCA Len TTA GAG Glu



2042 448	2084 462	2126 476	2168 490	2210 504	2252 518	2294 532	2336 546
ACA Thr	GAA Glu	TGC Cys	AAG	TCT Ser	CCA Pro	CCT	GAC Asp
TTC Phe	GCG Ala	CGC Arg	GAG	ATG Met	TTG Leu	CAA Gln	GAT Asp
$\texttt{GGC}\\ \texttt{G1}\underline{\mathtt{y}}$	CAA Gln	GTG Val	CCC	TCC Ser	CAC His	TTG Leu	TCA Ser
TCA Ser	$\mathtt{TAC}$	AAT Asn	AGC	$\mathtt{TAC}$	TCT Ser	GCT Ala	TTC
AAG Lys	TTT Phe	GTG Val	AGG Arg	GGC Gly	CTC	CTG	ATG Met
$\mathtt{ACC}$	$\mathtt{TAC}$	CCT Pro	GAG	GCT Ala	$\mathtt{TAT}$	GAA Glu	GAG Glu
ATC Ile	$\mathtt{TAC}$	CAC His	CTG	ATT	AGA Arg	$^{ m TGT}$	CTA Leu
CCC Pro	TGT Cys	CTG Leu	AGC	GAG	CAC His	ATC Ile	ACC Thr
GAA Glu	CCT	TTC Phe	GGC G1y	GTG	CGT Arg	AGC Ser	GAA Glu
CAG Gln	TCT Ser	ATG Met	TAC	GTG	CAG Gln	TTC Phe	AAG Lys
CAG Gln	AGC Ser	CAT His	GAG	ACT Thr	CGA Arg	GAG Glu	TCT
AGC Ser	AGC Ser	CAG Gln	CGG	TCA GCA Ser Ala	GTT Val	TGT Cys	GTC Val
TCC	CTC	GGA Gly	GTG	TCA	GAT Asp	ACC Thr	GTG Val
GAG Glu	CGC Arg	GAT Asp	CTC	ATC Ile	GAG Glu	CTC	CCT

2378 560 GAG Glu CGG Arg GCT Ala AAG LysAAG LysCAA Gln Arg CGC CAG Gln Ard CGI AAA LysAGG Arq AAG LysGAG Glu ATT

2420 574 LysAAG AAC Asn GAG Glu Glu GAG ATA Ile Glu GAG Ile ATT AGG Arg CGC Arg GAG Glu CGC CGA Ard Ard CGC Ard GAA Glu

2462 588 AAT Asn Glu GAG CIC Leu Pro CCC Ile ATT His CAC GIC Val Glu GAA Pro CCA TAC TyrAAG LysG1yGGC Gln CAG AAA Lys 2504  $_{
m LCL}$ Ser  $_{
m LCC}$ Ser  $_{
m LGC}$ CysACC  $\operatorname{Thr}$ TAT Tyr $_{
m LCI}$ Ser AAT Asn  $_{
m LLC}$ Phe GCC Ala CCIPro TTTPhe CAG Gln CAG Gln CTA Leu

2546 616 GCC Ala GGG G1yCAT His GlyGGC GAG Glu ACC  $\operatorname{Thr}$ AGC Ser ACC  $\operatorname{Thr}$ CCC Pro GGTGly TTGLeu GCT Ala  $_{
m LCL}$ Ser Asp GAT

2588 630 GCA Ala HisCAT Ser  $_{
m LCC}$ GGI G1yCCA Pro Ser AGT AGA Arg AGC Ser CTCLen Pro CCI $_{\rm ICI}$ Ser ATT Ile JCC Ser CIC Leu

2630 644 GGC GlyCAG Gln AGT Ser gcc Ala ACT  $\operatorname{Thr}$ CCC Pro TCASer CIGLeu CCI $\operatorname{Pro}$ ACC Thr CIG Len CIG Len TTTPhe GAC Asp

2672 658 CCC Pro  $_{
m LCL}$ Ser Asp GAC Glu GAA GAA Glu CIGLen AGT Ser GGG Gly GLL Val  $\mathrm{T}\mathrm{G}\mathrm{C}$ Cys  $_{
m LLC}$ Phe TCA Ser CCC Pro AGT Ser

AAG AAA GAT GAG AAC 2756 Lys Lys <u>Asp Glu Asn</u> 686		AGC GAC GGG GAG AGT 2798 Ser Asp Gly Glu Ser 700	AGT TTT CAA AAT TCC 2840 Ser Phe Gln Asn Ser 714	TTC ATG AAA CTG GAC ACA 2882 Phe Met Lys Leu Asp Thr 728	GAG AAA GGA GGA AAG 2924 Glu Lys Gly Gly Lys 742	CTG TTC AGC ACC TCA 2966 Leu Phe Ser Thr Ser 756	CCCAGGCTAC CTTCTCCATC 3013
CCA		GAC	CCC	TTC	GAA Glu	CTC	
	GCT	GTG	GTG CCC Val Pro	GCC Ala	TCT	AAG Lys	CACTACTGG
	ACT Thr	CCT	CCT	GCA Ala	CTC	CAG Gln	CACI
	AAA Lys	GCC Ala	GTT Val	GAA Glu	CCC	AAA Lys	TGA (
	CCC Pro	CCT	CGT	ATT Ile	GAT Asp	CAG	AAG Lys
)	TGG Trp	CCT	GAC	GCT Ala	TCA Ser	AAA Lys	$\mathtt{ACC}$
)	GTG Val	GTT Val	TCA Ser	TC AGC CAA GCT the Ser Gln Ala	ACT Thr	AGA AAA AAA Arg Lys Lys	CAC His
1	GAT Asp	TTA	AAT Asn	AGC	cca GCT Pro Ala		GTC Val
ne	3CA 11a	AGC Ser	3AT ASP	TC	CCA	AAA	JTC /

3063	3113	3163	3205
TGGCTGCTGT	GGAGGGGGTT	TGTATTTCC	AG
TGGTTTTTGT TTTTGTTTTT TTTTCCCCCA TGCTTTTGTT TGGCTGCTGT 3063	TTTGAGTT TGAACACATT AGCTCTGGGG GGAGGGGGTT 3113	GGGGGAAC CAAGAAATT TTAAATACAG TGTATTTTCC 3163	AGCTTCCTGT CTTTACACCA AAATAAAGTA TTGACACAAG AG
TTTTCCCCCA	TGAACACATT	CAAGAAAATT	AAATAAAGTA
TTTTGTTTTT	TATTTGAGTT	GAGGGGGAAC	CTTTACACCA
TGGTTTTTGT	AATTTTTAAG TA	TCCACAATGT GA	AGCTTCCTGT

C	СН	ט	,	ט	
CPICLYPPTAAKITR	CGHI	FCWACIL	HYLSLSEK TWSKCPI	TWSKCPIC	(UC332)
CPICLELIKEPVSTK	CDHI	FCKFCML	KLLNOKK	SPSQCPLC	(BRCA1)
CPICLELLKEPVSAD	CINHS	FCRACITL	NYESNRNTI	GKGNCPVC	(rpt-1)
CAFCHSVLHNPHOTG	CGHR	FCQQCIR	SIRELN	RELNSVPICPVC	(Traf5)
CPICMESFIEE OIRPKLLH	CGHT	ICROCLE	KLLASSI	NGVRCPFC	(HT2A)
RNPSL	CGHT	LCESCVD	LLFVR	GAGNCPEC	(MAT1)
CPVCLQYFAEPMMLD	CGHIN	ICCACLA	RCWGTAE	TINVSCPOC	(rfp)
<u>QVLQGGYFIDATTIIE</u>	O H H H	SCKTCIV	RYLE	TSKYCPIC	(bmi-1)
CALCIDEYEDGDKLRILP	CISHIA)	THICK CIVDE	M	TKKTCPVC	(CRZF)
GLICKENPIDSVLYM	CGHIM	MCVDCAI	EQWRGV	GGGCCPLC	(neu)

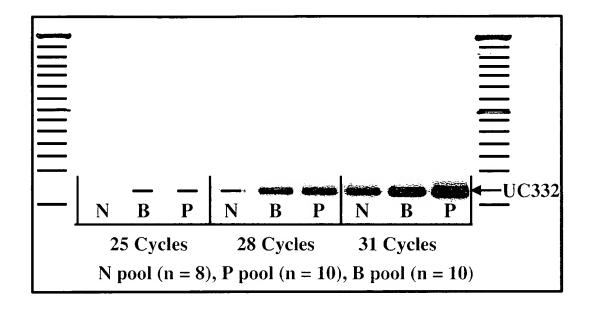


FIG. 13A

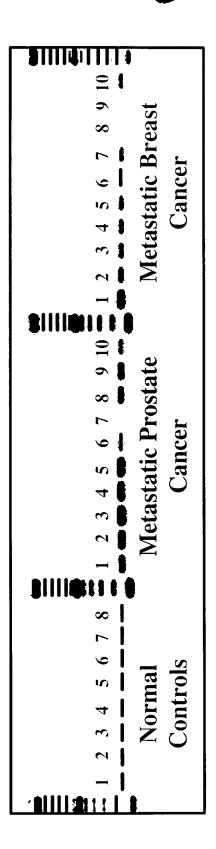


FIG. 13B

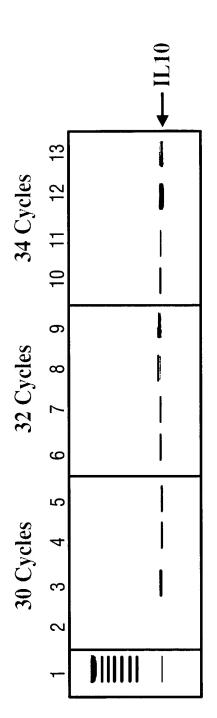


FIG. 14